Applicant specifically wishes to call the prior art MacConnell patent (USP 4,787,963) to the Examiner's attention. The MacConnell patent discloses methods and apparatus for forming various complexes, expressly said to include a sandwich complex. This complex is both subject to an attractive field for annealing the complex and a repulsive field for electronic washing of the complex. For example, at column 3, starting at line 7, the specification of MacConnell provides that:

> "A second labeled DNA or RNA probe which is complimentary to the filter-bound sample targets sequences, that is non-overlapping with the first filter-bound probe, is then annealed to the sample target sequences and thereby also becomes bound to the filter. Each resultant bound sandwich nucleic acid complex contains the first probe bound to the filter, the target sample nucleic acid sequence annealed to the first probe, and the second labeled probe annealed to the overhanging ends of the target nucleic acid sequence."

Should Konrad's claim be patentable over this art, the equivalent claim support by Applicant's disclosure would be patentable. However, Applicant is not contending that the claims in Konrad or the instant claims are patentably distinct from the prior art MacConnell patent.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "**Version with markings to show changes made.**"

Applicants submit herewith a paper and identical electronic copy of the Sequence Listing for the above patent application, in compliance with 37 CFR 1.821-1.825. As noted above, the Sequence Listing adds no new matter, and the computer readable copy is identical to the paper copy. Please amend the specification to replace the previously submitted sequence listing with the sequence listing submitted herewith.

If any minor issues remain, please contact Applicants' undersigned representative at 949-567-2300.

Respectfully submitted,

LYON & LYON LLP

Dated: August 6, 2001

By: _____
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"**Version with markings to show changes made**"

In the Title:

The title has been amended to Method for the Electronic Analysis of a Sample Oligonucleotide Sequence.

In the Specification:

The specification has been amended as follows:

Page 40, lines 19-32:

The following oligomers contain 3' ribonucleoside termini (U):

ET12R 5'- GCT AGC CCC TGC TCA TGA GTC TCU (Sequence ID No. 1)

CP-1 5'- AAA AAA AAA AAA AAA AAA AAU (Sequence ID No. 2)

AT-A1 5'- CTA CGT GGA CCT GGA GAG GAA GGA GAC TGC CTG U (Sequence ID No. 3)

AT-A2 5'- GAG TTC AGC AAA TTT GGA GU (Sequence ID No. 4)

AT-A3 5'- CGT AGA ACT CCT CAT CTC CU (Sequence ID No. 5)

AT-A4 5'- GTC TCC TTC CTC TCC AGU (Sequence ID No. 6)

AT-A5 5'- GAT GAG CAG TTC TAC GTG GU (Sequence ID No. 7)

AT-A6 5'- CTG GAG AAG AAG GAG ACU (Sequence ID No. 8)

AT-A7 5'- TTC CAC AGA CTT AGA TTT GAC U (Sequence ID No. 9)

AT-A8 5'- TTC CGC AGA TTT AGA AGA TU (Sequence ID No. 10)

AT-A9 5'- TGT TTG CCT GTT CTC AGA CU (Sequence ID No. 11)

AT-A10 5'- CAT CGC TGT GAC AAA ACA TU (Sequence ID No. 12)

At page 41, lines 11-26:

The following oligomers contain 5' amino termini:

ET21A 5'- Aminolink2 - TGC GAG CTG CAG TCA GAC AT (Sequence ID No. 13)

ET10AL 5'- Aminolink2 - GAG AGA CTC ATG AGC AGG (Sequence ID No. 14)

ET11AL 5'- Aminolink2 - CCT GCT CAT GAG TCT CTC (Sequence ID No. 15)

T2 5'- Aminolink2 - TTT TTT TTT TTT TTT TTT TT (Sequence ID No. 16)

RC-A1 5'- Aminolink2 - CAG GCA GTC TCC TTC CTC TCC AGG TCC ACG TAG (Sequence ID No. 17)

RC-A2 5'- Aminolink2 - CTC CAA ATT TGC TGA ACT C (Sequence ID No. 18)

RC-A3 5'- Aminolink2 - GGA GAT GAG GAG TTC TAC G (Sequence ID No. 19)

RC-A4 5'- Aminolink2 - CTG GAG AGG AAG GAG AC (Sequence ID No. 20)

RC-A5 5'- Aminolink2 - CCA CGT AGA ACT GCT CAT C (Sequence ID No. 21)

RC-A6 5'- Aminolink2 - GTC TCC TTC TTC TCC AG (Sequence ID No. 22)

RC-A7 5'- Aminolink2 - GTC AAA TCT AAG TCT GTG GAA (Sequence ID No. 23)

RC-A8 5'- Aminolink2 - ATC TTC TAA ATC TGC GGA A (Sequence ID No. 24)

RC-A9 5'- Aminolink2 - GTC TGA GAA CAG GCA AAC A (Sequence ID No. 25)

RC-A10 5'- Aminolink2 - ATG TTT TGT CAC AGC GAT G (Sequence ID No. 26)

Page 52, lines 27-31:

Ras-G 5'- GGT GGT GGG CGC CGG CGG TGT GGG CAA GAU -3' (Sequence ID No. 27)

Ras-1 3'- CC GCG GCC GCC ACA C - Aminolink2 -5' (Sequence ID No. 28)

Ras-2 3'- CC GCG GCA GCC ACA C - Aminolink2 -5' (Sequence ID No. 29)

Ras-3 3'- CC GTG GCA GCC ACA C - Aminolink2 -5' (Sequence ID No. 30)

Ras-T 5'- GGT GGT GGG CGC CGT CGG TGT GGG CAA GAU -3' (Sequence ID No. 31)

In the Claims:

49. A method for analyzing a sample oligonucleotide sequence comprising:

(a) contacting a said sample oligonucleotide sequence with an anchor sequence comprising an oligonucleotide sequence which is immobilized to a support and which hybridizes with said sample oligonucleotide sequence and with a probe comprising an oligonucleotide sequence which hybridizes to a target oligonucleotide sequence to be detected in a suitable buffer to form a complex;

(b) subjecting said complex to a field which moves unbound oligonucleotide sequences away from said anchor sequence in the direction of said field, wherein said field is ~~a magnetic field and a magnetic particle is attached to said sample oligonucleotide sequence or said probe or said field is~~ an electric field; and

(c) determining whether said probe is bound to said sample oligonucleotide sequence.

58. The method of claim 49 wherein said probe is from about 4 6 to about 100bases.